



0590  
1011

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/816,653

Source: ~ OIPE

Date Processed by STIC: 10/17/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

P.5

## RAW SEQUENCE LISTING

DATE: 10/17/2001

PATENT APPLICATION: US/09/816,653

TIME: 15:43:39

Input Set : A:\Sequence listing 09.816653--10716.57.txt

Output Set: N:\CRF3\10172001\I816653.raw

3 <110> APPLICANT: Rastelli, Luca  
 4 Pennica, Diane  
 6 <120> TITLE OF INVENTION: NOVEL HUMAN STRA6-LIKE PROTEIN AND NUCLEIC ACIDS ENCODING  
 THE SAME

**Does Not Comply  
 Corrected Diskette Needed**

*Errors on pp. 3-4*

8 <130> FILE REFERENCE: 10716/57  
 10 <140> CURRENT APPLICATION NUMBER: 09/816653  
 11 <141> CURRENT FILING DATE: 2001-03-23  
 13 <150> PRIOR APPLICATION NUMBER: 60/191,532  
 14 <151> PRIOR FILING DATE: 2000-03-23  
 16 <160> NUMBER OF SEQ ID NOS: 7  
 18 <170> SOFTWARE: PatentIn version 3.1  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 598  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Homo sapiens hSTRA6 nucleotide fragment, 5' region  
 25 <220> FEATURE:  
 26 <221> NAME/KEY: misc\_feature  
 27 <222> LOCATION: (92)..(92)  
 28 <223> OTHER INFORMATION: n is a, t, c or g  
 31 <220> FEATURE:  
 32 <221> NAME/KEY: misc\_feature  
 33 <222> LOCATION: (93)..(93)  
 34 <223> OTHER INFORMATION: n is a, t, c or g  
 37 <400> SEQUENCE: 1  
 38 atgtcccagc cagcagggaa ccagacctcc cccggggcca cagaggacta ctccatggc 60  
 W--> 40 agctgggtaca tcgatgagcc ccaggggggg gnnagagctcc agccagaggg ggaagtggcc 120  
 42 tctgcccaca ccagcatacc accgggcttg taccacgctt gcctggcctc gctgtcaatc 180  
 44 cttgtgctgc tgcctctggc catgctggtg aggcgccgcc agctctggcc tgactgtgtg 240  
 46 cgtggcaggc ccggcctgcc cagccctgtg gatttcttgg ctggggacag gccccgggca 300  
 48 gtgcctgctg ctgttttcat ggtcctcttg agctccctgt gtttgcctgc ccccgacgag 360  
 50 gacgcattgc ccttcctgac tctgcctca gcacccagcc aagatgggaa aactgaggct 420  
 52 ccaagagggg cctggaagat actgggactg ttccattatg ctgccctcta ctaccctctg 480  
 54 gctgcctgtg ccacggctgg ccacacagct gcacacctgc tcggcagcac gctgtcctgg 540  
 56 gccacacctg ggtccagggt ctggcagagg gcagagtgtc cccaggtgcc caagatct 598  
 59 <210> SEQ ID NO: 2  
 60 <211> LENGTH: 199  
 61 <212> TYPE: PRT  
 62 <213> ORGANISM: Homo sapiens hSTRA6 amino terminal polypeptide fragment  
 64 <220> FEATURE:  
 65 <221> NAME/KEY: MISC\_FEATURE  
 66 <222> LOCATION: (31)..(31)  
 67 <223> OTHER INFORMATION: Xaa is any amino acid  
 70 <400> SEQUENCE: 2  
 72 Met Ser Gln Pro Ala Gly Asn Gln Thr Ser Pro Gly Ala Thr Glu Asp  
 73 1 5 10 15  
 W--> 76 Tyr Ser Tyr Gly Ser Trp Tyr Ile Asp Glu Pro Gln Gly Gly Xaa Glu  
 77 20 25 30  
 80 Leu Gln Pro Glu Gly Glu Val Pro Ser Cys His Thr Ser Ile Pro Pro

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Input Set : A:\Sequence listing 09.816653--10716.57.txt

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```

81          35          40          45
84 Gly Leu Tyr His Ala Cys Leu Ala Ser Leu Ser Ile Leu Val Leu Leu
85          50          55          60
88 Leu Leu Ala Met Leu Val Arg Arg Arg Gln Leu Trp Pro Asp Cys Val
89 65          70          75          80
92 Arg Gly Arg Pro Gly Leu Pro Ser Pro Val Asp Phe Leu Ala Gly Asp
93          85          90          95
96 Arg Pro Arg Ala Val Pro Ala Ala Val Phe Met Val Leu Leu Ser Ser
97          100          105          110
100 Leu Cys Leu Leu Leu Pro Asp Glu Asp Ala Leu Pro Phe Leu Thr Leu
101          115          120          125
104 Ala Ser Ala Pro Ser Gln Asp Gly Lys Thr Glu Ala Pro Arg Gly Ala
105          130          135          140
108 Trp Lys Ile Leu Gly Leu Phe His Tyr Ala Ala Leu Tyr Tyr Pro Leu
109 145          150          155          160
112 Ala Ala Cys Ala Thr Ala Gly His Thr Ala Ala His Leu Leu Gly Ser
113          165          170          175
116 Thr Leu Ser Trp Ala His Leu Gly Val Gln Val Trp Gln Arg Ala Glu
117          180          185          190
120 Cys Pro Gln Val Pro Lys Ile
121          195
124 <210> SEQ ID NO: 3
125 <211> LENGTH: 1351
126 <212> TYPE: DNA
127 <213> ORGANISM: Homo sapiens hSTRA6 nucleotide fragment, 3' region
129 <220> FEATURE:
130 <221> NAME/KEY: misc_feature
131 <222> LOCATION: (437)..(437)
132 <223> OTHER INFORMATION: n is a, t, c or g
135 <220> FEATURE:
136 <221> NAME/KEY: misc_feature
137 <222> LOCATION: (438)..(438)
138 <223> OTHER INFORMATION: n is a, t, c or g
141 <220> FEATURE:
142 <221> NAME/KEY: misc_feature
143 <222> LOCATION: (439)..(439)
144 <223> OTHER INFORMATION: n is a, t, c or g
147 <220> FEATURE:
148 <221> NAME/KEY: misc_feature
149 <222> LOCATION: (440)..(440)
150 <223> OTHER INFORMATION: n is a, t, c or g
153 <220> FEATURE:
154 <221> NAME/KEY: misc_feature
155 <222> LOCATION: (441)..(441)
156 <223> OTHER INFORMATION: n is a, t, c or g
159 <220> FEATURE:
160 <221> NAME/KEY: misc_feature
161 <222> LOCATION: (442)..(442)
162 <223> OTHER INFORMATION: n is a, t, c or g

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Input Set : A:\Sequence listing 09.816653--10716.57.txt

Output Set: N:\CRF3\10172001\I816653.raw

165 <220> FEATURE:  
166 <221> NAME/KEY: misc\_feature  
167 <222> LOCATION: (694)..(694)  
168 <223> OTHER INFORMATION: n is a, t, c, or g  
171 <220> FEATURE:  
172 <221> NAME/KEY: misc\_feature  
173 <222> LOCATION: (867)..(867)  
174 <223> OTHER INFORMATION: n is a, t, c, or g  
177 <220> FEATURE:  
178 <221> NAME/KEY: misc\_feature  
179 <222> LOCATION: (874)..(874)  
180 <223> OTHER INFORMATION: n is a, t, c or g  
183 <220> FEATURE:  
184 <221> NAME/KEY: misc\_feature  
185 <222> LOCATION: (905)..(905)  
186 <223> OTHER INFORMATION: n is a, t, c or g  
189 <220> FEATURE:  
190 <221> NAME/KEY: misc\_feature  
191 <222> LOCATION: (908)..(908)  
192 <223> OTHER INFORMATION: n is a, t, c or g  
195 <220> FEATURE:  
196 <221> NAME/KEY: misc\_feature  
197 <222> LOCATION: (1155)..(1155)  
198 <223> OTHER INFORMATION: n is a, t, c or g  
201 <220> FEATURE:  
202 <221> NAME/KEY: misc\_feature  
203 <222> LOCATION: (1172)..(1172)  
204 <223> OTHER INFORMATION: n is a, t, c or g  
207 <220> FEATURE:  
208 <221> NAME/KEY: misc\_feature  
209 <222> LOCATION: (1174)..(1174)  
210 <223> OTHER INFORMATION: n is a, t, c or g  
213 <220> FEATURE:  
214 <221> NAME/KEY: misc\_feature  
215 <222> LOCATION: (1197)..(1197)  
216 <223> OTHER INFORMATION: n is a, t, c or g  
219 <220> FEATURE:  
220 <221> NAME/KEY: misc\_feature  
221 <222> LOCATION: (1198)..(1198)  
222 <223> OTHER INFORMATION: n is a, t, c or g  
225 <220> FEATURE:  
226 <221> NAME/KEY: misc\_feature  
227 <222> LOCATION: (1204)..(1204)  
228 <223> OTHER INFORMATION: n is a, t, c or g  
231 <220> FEATURE:  
232 <221> NAME/KEY: misc\_feature  
233 <222> LOCATION: (1295)..(1295)  
234 <223> OTHER INFORMATION: n is a, t, c or g  
237 <400> SEQUENCE: 3

location 1197 is not n

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TIME: 15:43:39

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Output Set: N:\CRF3\10172001\I816653.raw

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238 tgetacatct cagccttggt cttgtcctgc ttactcaoct tectggtcct gatgcgctca      60
240 ctggtgacac acaggcttgg ttctgggggc agcggggatg gccagttttc atggaacctg      120
242 ttttctgtcc ccctgccact cccgcccctg gcagggtctc tgggtgcagca gatcatcttc      180
244 ttctctggga ccacggccct ggcttccctg gtgctcatgc ctgtgctcca tggcaggaac      240
246 ctctgtttct tccgttccct ggagtcctcg tggcccttct ggctgacttt ggccttggt      300
248 gtgatcctgc agaacatggc agcccattgg gtcttctctg agactcatga tggacaccca      360
250 cagctgacca accggcgagt getctatgca gccacctttc ttctcttccc cctcaatgtg      420
W--> 252 ctggtgggtg ccattggnnnn nncctgctcc cccagcattg ccattccgcca cccaccccca      480
254 ggctactaca cgtaccgaaa cttcttgaag attgaagtca gccagtcgca tccagccatg      540
256 acagccttct gctccctgct cctgcaagcg cagagcctcc taccaggac catggcagcc      600
258 cccagggaca gcctcagacc aggggaggaa gacgaaggat gcagctgcta cagacaaagg      660
W--> 260 actccatggc caaggagct agggccgggg ccancgcgg cagggtctgc tggggtctgg      720
262 cctacacgct gctgcacaac ccaaccctgc aggtcttccg caagacggcc ctgttgggtg      780
264 ccaatggtgc ccagccctgc tctcctctcc ccggtctctc tcccagcatc acaccagcca      840
W--> 266 tgcagccagc aggtcctccg gatcacngtg gttnggtgga ggtctgtctg cactgggagc      900
W--> 268 ctctganggg ctctgtctca cccacttgcc tatgggagag ccagcagggg ttctggagaa      960
270 aaaaactggg gggttagggc cttggtccag gagccagttg agccagggca gccacatcca     1020
272 ggctctctcc taccctgggt ctgccatcag ccttgaaggg cctcgatgaa gccttctctg     1080
274 gaaccactcc agcccagctc cacctcagcc ttggccttca cgctgtggaa gcagccaagg     1140
W--> 276 cacttctcta cccntcagc gccacggacc tntntgggga gtggccggaa agctctcngg     1200
W--> 278 cctntggcct gcagggcagc ccaagtcag actcagacca ggtcccacac tgagctgccc     1260
W--> 280 acactcgaga gccagatatt tttgtagttt ttatnccitt ggctattatg aaagaggtta     1320
282 gtgtgttccc tgcaataaac ttgttcttga g                                     1351
285 <210> SEQ ID NO: 4
286 <211> LENGTH: 325
287 <212> TYPE: PRT
288 <213> ORGANISM: Homo sapiens hSTRA6 polypeptide fragment, carboxy terminus
290 <220> FEATURE:
291 <221> NAME/KEY: MISC_FEATURE
292 <222> LOCATION: (146)..(148)
293 <223> OTHER INFORMATION: Xaa represents any amino acid, other, or unkown
296 <220> FEATURE:
297 <221> NAME/KEY: MISC_FEATURE
298 <222> LOCATION: (232)..(232)
299 <223> OTHER INFORMATION: Xaa represents any amino acid, other, or unkown
302 <220> FEATURE:
303 <221> NAME/KEY: MISC_FEATURE
304 <222> LOCATION: (290)..(290)
305 <223> OTHER INFORMATION: Xaa represents any amino acid, other, or unkown
308 <220> FEATURE:
309 <221> NAME/KEY: MISC_FEATURE
310 <222> LOCATION: (292)..(292)
311 <223> OTHER INFORMATION: Xaa represents any amino acid, other, or unkown
314 <220> FEATURE:
315 <221> NAME/KEY: MISC_FEATURE
316 <222> LOCATION: (302)..(302)
317 <223> OTHER INFORMATION: Xaa represents any amino acid, other, or unkown
320 <220> FEATURE:
321 <221> NAME/KEY: MISC_FEATURE

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Output Set: N:\CRF3\10172001\I816653.raw

322 &lt;222&gt; LOCATION: (303)..(303)

323 &lt;223&gt; OTHER INFORMATION: Xaa represents any amino acid, other, or unknown

326 &lt;400&gt; SEQUENCE: 4

328 Cys Tyr Ile Ser Ala Leu Val Leu Ser Cys Leu Leu Thr Phe Leu Val

329 1 5 10 15

332 Leu Met Arg Ser Leu Val Thr His Arg Leu Gly Ser Gly Gly Ser Gly

333 20 25 30

336 Asp Gly Gln Phe Ser Trp Asn Leu Phe Ser Val Pro Leu Pro Leu Pro

337 35 40 45

340 Pro Leu Ala Gly Leu Leu Val Gln Gln Ile Ile Phe Phe Leu Gly Thr

341 50 55 60

344 Thr Ala Leu Ala Phe Leu Val Leu Met Pro Val Leu His Gly Arg Asn

345 65 70 75 80

348 Leu Leu Phe Phe Arg Ser Leu Glu Ser Ser Trp Pro Phe Trp Leu Thr

349 85 90 95

352 Leu Ala Leu Ala Val Ile Leu Gln Asn Met Ala Ala His Trp Val Phe

353 100 105 110

356 Leu Glu Thr His Asp Gly His Pro Gln Leu Thr Asn Arg Arg Val Leu

357 115 120 125

360 Tyr Ala Ala Thr Phe Leu Leu Phe Pro Leu Asn Val Leu Val Gly Ala

361 130 135 140

W--&gt; 364 Met Xaa Xaa Xaa Cys Ser Pro Ser Ile Ala Ile Arg His Pro Thr Pro

365 145 150 155 160

368 Gly Tyr Tyr Thr Tyr Arg Asn Phe Leu Lys Ile Glu Val Ser Gln Ser

369 165 170 175

372 His Pro Ala Met Thr Ala Phe Cys Ser Leu Leu Leu Gln Ala Gln Ser

373 180 185 190

376 Leu Leu Pro Arg Thr Met Ala Ala Pro Gln Asp Ser Leu Arg Pro Gly

377 195 200 205

380 Glu Glu Asp Glu Gly Met Gln Leu Leu Gln Thr Lys Asp Ser Met Ala

381 210 215 220

W--&gt; 384 Lys Gly Ala Arg Pro Gly Ala Xaa Arg Gly Arg Ala Arg Trp Gly Leu

385 225 230 235 240

388 Ala Tyr Thr Leu Leu His Asn Pro Thr Leu Gln Val Phe Arg Lys Thr

389 245 250 255

392 Ala Leu Leu Gly Ala Asn Gly Ala Gln Pro Cys Ser Ser Leu Pro Gly

393 260 265 270

396 Ser Pro Pro Ser Ile Thr Pro Ala Met Gln Pro Ala Gly Pro Pro Asp

397 275 280 285

W--&gt; 400 His Xaa Gly Xaa Val Glu Val Cys Leu His Trp Glu Pro Xaa Xaa Gly

401 290 295 300

404 Ser Ala Pro Pro Thr Trp Leu Trp Glu Ser Gln Gln Gly Phe Trp Arg

405 305 310 315 320

408 Lys Lys Leu Val Gly

409 325

412 &lt;210&gt; SEQ ID NO: 5

413 &lt;211&gt; LENGTH: 6964

414 &lt;212&gt; TYPE: DNA

415 <213> ORGANISM: Homo sapiens clone RP11-60L3, Sequencing in Progress, 9 unordered pieces; GenBank AC023300, nts 150524 to 157487

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/816,653

DATE: 10/17/2001

TIME: 15:43:40

Input Set : A:\Sequence listing 09.816653--10716.57.txt

Output Set: N:\CRF3\10172001\I816653.raw

L:40 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:276 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:364 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:440 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5